

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2003, 01:47:25 ; Search time 237 Seconds

(Without alignments)
5311.675 Million cell updates/sec

Title: US-09-867-958-2

Perfect score: 559

Sequence: 1 ccgcacatgcgcgcgcgcgcac.....cgcctagccttgctgcgcg 559

Scoring table: IDENTITY_NDC

Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
23:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
24:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	100.0	559	20	AA36136
2	549.4	98.3	1006	22	AA158712
3	434.6	77.7	1859	22	AAK55488
4	432.2	77.3	1869	22	AA158813
5	381.8	68.3	1074	22	AA160498
6	103	18.4	2007	22	ABQ54845
7	102.6	18.4	764	22	AA197619
8	101.2	18.1	483	22	AAH43100
9	94.2	16.9	569	24	ABQ58935

10	94.2	16.9	664	24	ABQ57521	Human colon cancer
11	93	16.6	570	24	ABL37927	Human colon tumour
12	84.4	15.1	575	24	ABQ59145	Human colon cancer
13	82.6	14.8	561	24	ABQ58126	Human colon cancer
14	75.2	13.5	473	24	ABK09599	Human ovarian tumor
15	65.4	11.7	471	24	ABN88218	Human colon cancer
16	56.6	10.1	1776	24	ABL39694	Human NS cDNA sequ
17	54.4	9.7	314	22	AAFA9993	Nucleic acid sequ
18	50.4	9.0	477	21	AAE21984	Human breast and o
19	48.8	8.7	477	22	AA182544	Human polynucleoti
20	45.2	8.1	587	21	AAAC06253	Human prostate exp
21	39	7.0	441	23	ABV17722	Human prostate exp
22	39	7.0	497	23	ABV47515	Human prostate exp
23	38.2	6.8	2418	23	ABL03387	Drosophila melanog
24	38.2	6.8	4204	23	ABL04694	Drosophila melanog
25	38.2	6.8	4477	23	ABL03386	Drosophila melanog
26	35.2	6.3	301	24	ABK93035	cDNA encoding huma
27	35.2	6.3	3929	23	AA570024	DNA encoding novel
28	35.2	6.3	3933	16	AA03885	Human mucosal
29	34.6	6.2	467	22	ABA51936	Human foetal
30	34.6	6.2	467	22	ABA21751	Probe #217 for
31	34.6	6.2	467	22	AAK00225	Human brain expres
32	34.6	6.2	467	22	AAK25668	Human bone marrow
33	34.6	6.2	467	22	AA110295	Probe #228 for gen
34	34.6	6.2	467	22	AA13544	Probe #230 used to
35	34.6	6.2	467	22	AA100231	Probe #222 used to
36	34.6	6.2	467	22	ABA00240	Human genome-deriv
37	34.6	6.2	1186	22	ABA66719	Human breast cell
38	34.6	6.2	1186	22	ABA64595	Human foetal liver
39	34.6	6.2	1186	22	ABA31721	Probe #10187 for g
40	34.6	6.2	1186	22	AAK13036	Human brain expres
41	34.6	6.2	1186	22	AAK38767	Human bone marrow
42	34.6	6.2	1186	22	AA119573	Probe #9506 for ge
43	34.6	6.2	1186	22	AA144765	Probe #13451 used
44	34.6	6.2	1186	22	AA105293	Probe #5284 used t
45	34.6	6.2	1186	24	AB512841	Human genome-deriv

ALIGNMENTS

Sequence A

RESULT 1
ID AAX36136 standard; DNA: 559 BP.
AC AAX36136;
XX
XX 19-JUL-1999 (first entry)
DE
XX DNA encoding a human progesterone receptor complex p23-like protein.
XX
XX Human progesterone receptor complex p23-like protein; PR33P;
KW neurological disorder; antagonist; reproductive disorder;
KW immunological disorder; neoplastic disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX W09919483-A1.
XX
XX 22-APR-1999.
XX
XX 09-OCR-1998; 98WO-US21402.
XX
XX 09-OCR-1997; 97US-0948197.
XX
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Corley NC, Shah P, Yue H;
XX
XX WPI: 1999-302530/25.
XX
XX P-PSDB; AAY02591.
XX
XX Human progesterone receptor complex p23-like protein
XX
XX PT

C. GUN

